

SEQUENCE LISTING

<110> Japan Science and Technology Corporation

<120> Human nucleoprotein having a WW domain and
a polynucleotide encoding the protein

<130> 00-F-061PCT

<140> PCT/JP00/08253

<141> 2000-11-22

<150> JP11-332572

<151> 1999-11-24

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 704

<212> PRT

<213> Homo sapiens

<400> 1

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09889722 404904

[illegible]

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 Phe Lys Tyr Ala Glu Ala Ala Arg Arg Leu Ile Glu Ser Arg Ser Ala
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 Ser Pro Asp Ser Arg Lys Val Val Lys Trp Asn Val Glu Asp Thr Phe
 305 310 315 320
 Ser Trp Leu Arg Lys Asp His Ser Ala Ser Lys Glu Asp Tyr Met Asp
 325 330 335
 Arg Leu Glu His Leu Arg Arg Gln Cys Gly Pro His Val Ser Ala Ala
 340 345 350
 Ala Lys Asp Ser Val Glu Gly Ile Cys Ser Lys Ile Tyr His Ile Ser
 355 360 365
 Leu Glu Tyr Val Lys Arg Ile Arg Glu Lys His Leu Ala Ile Leu Lys
 370 375 380
 Glu Asn Asn Ile Ser Glu Glu Val Glu Ala Pro Glu Val Glu Pro Arg
 385 390 395 400
 Leu Val Tyr Cys Tyr Pro Val Arg Leu Ala Val Ser Ala Pro Pro Met
 405 410 415
 Pro Ser Val Glu Met His Met Glu Asn Asn Val Val Cys Ile Arg Tyr
 420 425 430
 Lys Gly Glu Met Val Lys Val Ser Arg Asn Tyr Phe Ser Lys Leu Trp
 435 440 445
 Leu Leu Tyr Arg Tyr Ser Cys Ile Asp Asp Ser Ala Phe Glu Arg Phe
 450 455 460
 Leu Pro Arg Val Trp Cys Leu Leu Arg Arg Tyr Gln Met Met Phe Gly
 465 470 475 480
 Val Gly Leu Tyr Glu Gly Thr Gly Leu Gln Gly Ser Leu Pro Val His
 485 490 495
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0989722-101901
 106707-2276960

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Asp Thr Asp Gly Tyr Phe Gly Ser Arg Gly Pro Cys Leu Asp Phe Ala			
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Pro Leu Ser Gly Ser Phe Glu Ala Asn Pro Pro Phe Cys Glu Glu Leu			
545	550	555	560
Met Asp Ala Met Val Ser His Phe Glu Arg Leu Leu Glu Ser Ser Pro			
565	570	575	
Glu Pro Leu Ser Phe Ile Val Phe Ile Pro Glu Trp Arg Glu Pro Pro			
580	585	590	
Thr Pro Ala Leu Thr Arg Met Glu Gln Ser Arg Phe Lys Arg His Gln			
595	600	605	
Leu Ile Leu Pro Ala Phe Glu His Glu Tyr Arg Ser Gly Ser Gln His			
610	615	620	
Ile Cys Lys Lys Glu Glu Met His Tyr Lys Ala Val His Asn Thr Ala			
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Val Leu Phe Leu Gln Asn Asp Pro Gly Phe Ala Lys Trp Ala Pro Thr			
645	650	655	
Pro Glu Arg Leu Gln Glu Leu Ser Ala Ala Tyr Arg Gln Ser Gly Arg			
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<212> DNA

<213> Homo sapiens

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09889723 101901

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292).. (2406)

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 tccctgggc tccgtccac tccactgctg accagcccat tcgctgtgc tgagtcttcc 180
 tgcaggcctt tccttgctc tgtgggacc tgtgggggtc catccggctg gagaagaaaa 240
 gcctctcatg ctaacgttgc agacccaga gggtcctgtg tgggtgtgga g atg gcc 297

Met Ala

0909722-101901

1

aat gag aat cac ggc agc ccc cgg gag gaa gcg tcc ctg ctg agt cac 345
 Asn Glu Asn His Gly Ser Pro Arg Glu Glu Ala Ser Leu Leu Ser His
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 tcc cca ggt acc tcc aat cag agc cag ccc tgt tct cca aag cca atc 393
 Ser Pro Gly Thr Ser Asn Gln Ser Gln Pro Cys Ser Pro Lys Pro Ile
 20 25 30
 cgc ctg gtt cag gac ctc cca gag gag ctg gtg cat gca ggc tgg gag 441
 Arg Leu Val Gln Asp Leu Pro Glu Glu Leu Val His Ala Gly Trp Glu
 35 40 45 50
 aag tgc tgg agc cgg agg gag aat cgt ccc tac tac ttc aac cga ttc 489
 Lys Cys Trp Ser Arg Arg Glu Asn Arg Pro Tyr Tyr Phe Asn Arg Phe
 55 60 65
 acc aac cag tcc ctg tgg gag atg ccc gtg ctg ggg cag cac gat gtg 537
 Thr Asn Gln Ser Leu Trp Glu Met Pro Val Leu Gly Gln His Asp Val
 70 75 80
 att tcg gac cct ttg ggg ctg aat gcg acc cca ctg ccc caa gac tca 585
 Ile Ser Asp Pro Leu Gly Leu Asn Ala Thr Pro Leu Pro Gln Asp Ser
 85 90 95
 agc ttg gtg gaa act ccc ccg gct gag aac aag ccc aga aag cgg cag 633
 Ser Leu Val Glu Thr Pro Pro Ala Glu Asn Lys Pro Arg Lys Arg Gln
 100 105 110
 ctc tcg gaa gag cag cca agc ggc aat ggt gtg aag aag ccc aag att 681
 Leu Ser Glu Glu Gln Pro Ser Gly Asn Gly Val Lys Lys Pro Lys Ile
 115 120 125 130
 gaa atc cca gtg aca ccc aca ggc cag tcg gtg ccc agc tcc ccc agt 729
 Glu Ile Pro Val Thr Pro Thr Gly Gln Ser Val Pro Ser Ser Pro Ser
 135 140 145
 atc cca gga acc cca acg ctg aag atg tgg ggt acg tcc cct gaa gat 777

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 105707-2225950

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aaa cag cag gca gct ctc cta cga ccc act gag gtc tac tgg gac ctg	825
Lys Gln Gln Ala Ala Leu Leu Arg Pro Thr Glu Val Tyr Trp Asp Leu	
165	170
175	
gac atc cag acc aat gct gtc atc aag cac cgg ggg cct tca gag gtg	873
Asp Ile Gln Thr Asn Ala Val Ile Lys His Arg Gly Pro Ser Glu Val	
180	185
190	
ctg ccc ccg cat ccc gaa gtg gaa ctg ctc cgc tct cag ctc atc ctg	921
Leu Pro Pro His Pro Glu Val Glu Leu Leu Arg Ser Gln Leu Ile Leu	
195	200
205	210
aag ctt cgg cag cac tat cgg gag ctg tgc cag cag cga gag ggc att	969
Lys Leu Arg Gln His Tyr Arg Glu Leu Cys Gln Gln Arg Glu Gly Ile	
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Glu Pro Pro Arg Glu Ser Phe Asn Arg Trp Met Leu Glu Arg Lys Val	
230	235
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Val Asp Lys Gly Ser Asp Pro Leu Leu Pro Ser Asn Cys Glu Pro Val	
245	250
255	
gtg tca cct tcc atg ttt cgt gaa atc atg aac gac att cct atc agg	1113
Val Ser Pro Ser Met Phe Arg Glu Ile Met Asn Asp Ile Pro Ile Arg	
260	265
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tta tcc cga atc aag ttc cgg gag gaa gcc aag cgc ctg ctc ttt aaa	1161
Leu Ser Arg Ile Lys Phe Arg Glu Glu Ala Lys Arg Leu Leu Phe Lys	
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285	290
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Tyr Ala Glu Ala Ala Arg Arg Leu Ile Glu Ser Arg Ser Ala Ser Pro	
295	300
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Asp Ser Arg Lys Val Val Lys Trp Asn Val Glu Asp Thr Phe Ser Trp	
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Leu Arg Lys Asp His Ser Ala Ser Lys Glu Asp Tyr Met Asp Arg Leu	
325 330 335	
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Glu His Leu Arg Arg Gln Cys Gly Pro His Val Ser Ala Ala Ala Lys	
340 345 350	
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Asp Ser Val Glu Gly Ile Cys Ser Lys Ile Tyr His Ile Ser Leu Glu	
355 360 365 370	
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Tyr Val Lys Arg Ile Arg Glu Lys His Leu Ala Ile Leu Lys Glu Asn	
375 380 385	
aac atc tca gag gag gtg gag gcc cct gag gtg gag ccc cgc cta gtg	1497
Asn Ile Ser Glu Glu Val Glu Ala Pro Glu Val Glu Pro Arg Leu Val	
390 395 400	
tac tgc tac cca gtc cgg ctg gct gtg tct gca ccg ccc atg ccc agc	1545
Tyr Cys Tyr Pro Val Arg Leu Ala Val Ser Ala Pro Pro Met Pro Ser	
405 410 415	
gtg gag atg cac atg gag aac aac gtg gtc tgc atc cgg tat aag gga	1593
Val Glu Met His Met Glu Asn Asn Val Val Cys Ile Arg Tyr Lys Gly	
420 425 430	
gag atg gtc aag gtc agc cgc aac tac ttc agc aag ctg tgg ctc ctt	1641
Glu Met Val Lys Val Ser Arg Asn Tyr Phe Ser Lys Leu Trp Leu Leu	
435 440 445 450	
tac cgc tac agc tgc att gat gac tct gcc ttt gag agg ttc ctg ccc	1689
Tyr Arg Tyr Ser Cys Ile Asp Asp Ser Ala Phe Glu Arg Phe Leu Pro	

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cgg gtc tgg tgt ctt ctc cga cgg tac cag atg atg ttc ggc gtg ggc				1737
Arg Val Trp Cys Leu Leu Arg Arg Tyr Gln Met Met Phe Gly Val Gly				
	470	475	480	
ctc tac gag ggg act ggc ctg cag gga tcg ctg cct gtg cat gtc ttt				1785
Leu Tyr Glu Gly Thr Gly Leu Gln Gly Ser Leu Pro Val His Val Phe				
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gag gcc ctc cac cga ctc ttt ggc gtc agc ttc gag tgc ttc gcc tca				1833
Glu Ala Leu His Arg Leu Phe Gly Val Ser Phe Glu Cys Phe Ala Ser				
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ccc ctc aac tgc tac ttc cgc cag tac tgt tct gcc ttc ccc gac aca				1881
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Asp Gly Tyr Phe Gly Ser Arg Gly Pro Cys Leu Asp Phe Ala Pro Leu				
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agt ggt tca ttt gag gcc aac cct ccc ttc tgc gag gag ctc atg gat				1977
Ser Gly Ser Phe Glu Ala Asn Pro Pro Phe Cys Glu Glu Leu Met Asp				
	550	555	560	
gcc atg gtc tct cac ttt gag aga ctg ctt gag agc tca ccg gag ccc				2025
Ala Met Val Ser His Phe Glu Arg Leu Leu Glu Ser Ser Pro Glu Pro				
	565	570	575	
ctg tcc ttc atc gtg ttc atc cct gag tgg cgg gaa ccc cca aca cca				2073
Leu Ser Phe Ile Val Phe Ile Pro Glu Trp Arg Glu Pro Pro Thr Pro				
	580	585	590	
gcg ctc acc cgc atg gag cag agc cgc ttc aaa cgc cac cag ttg atc				2121
Ala Leu Thr Arg Met Glu Gln Ser Arg Phe Lys Arg His Gln Leu Ile				
	595	600	605	610
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Leu Pro Ala Phe Glu His Glu Tyr Arg Ser Gly Ser Gln His Ile Cys
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 Lys Lys Glu Glu Met His Tyr Lys Ala Val His Asn Thr Ala Val Leu
 630 635 640
 ttc cta cag aac gac cct ggc ttt gcc aag tgg gcg ccg acg cct gaa 2265
 Phe Leu Gln Asn Asp Pro Gly Phe Ala Lys Trp Ala Pro Thr Pro Glu
 645 650 655
 cgg ctg cag gag ctg agt gct gcc tac cgg cag tca ggc cgc agc cac 2313
 Arg Leu Gln Glu Leu Ser Ala Ala Tyr Arg Gln Ser Gly Arg Ser His
 660 665 670
 agc tct ggt tct tcc tca tgc tcc tcc tgc gag gcc aag gac cgg gac 2361
 Ser Ser Gly Ser Ser Ser Ser Ser Ser Ser Glu Ala Lys Asp Arg Asp
 675 680 685 690
 tgc ggc cgt gag cag ggt cct agc cgc gag cct cac ccc act taa 2406
 Ser Gly Arg Glu Gln Gly Pro Ser Arg Glu Pro His Pro Thr
 695 700 705
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<212> DNA

<213> Artificial sequence

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<213> Synthesized oligonucleotide

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<210> 5

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<212> DNA

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090921 10494

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<211> 33

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<220>

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33

090907 22/09/2009